Description

A98893 Sequence 1 A98895 Sequence 3 A98899 Sequence 7 A98899 Sequence 6 A95931 Sequence 6 AX014743 Sequence 9 AX014748 Sequence AX014748 Sequence AX014748 Sequence AX014748 Sequence AX014748 Sequence AX014748 Human ade

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9b\_ltg:\*
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Database

Post-processing:

Minimum DB Maximum DB

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AE008178 Agrobacte
AR036572 Sequence
AR036573 Sequence
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AL04264 Human DNA
AL149464 Human DNA
AL149464 Human DNA
AL0431737 Mus muscu
AC073172 Mus muscu
AC073124 Homo sapi
AC08134 Mus muscu
AC073124 Homo sapi
AC082167 Human sapi
AC08269 Homo sapi
AC0826742 Mus muscu
AC0826741 Human ade
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AC01558 Drosophil
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26-JAN-2000

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/db_xref="G1:6781857"
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GCYXKCTNRPF"
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Derose, R. and Hoffmann, J.
GENE CODING FOR ANDROCTONINE, VECTOR CONTAINING SAME AND TRANSFORMED DISEASE-RESISTANT PLANTS OBTAINED
PATCH: WO 9909149-A 3 25-FEB-1999;
DEROSE RICHARD (FR); HOFFMANN JULES (FR)
LOCALION/QUALIFIERS
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              /note="unnamed protein product"
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/organism="unidentified"
/db_xref="taxon:32644"
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Sequence 3 from Patent W09909189.
A98895 GI:6781856
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Sequence 7 from Patent W09909189.
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1 (bases 1 to 97)
Derose,R. and Hoffmann,J.
GENE CODING FOR AUDROCTONINE, VECTOR CONTAINING SAME AND
TRANSFORMED DISEASE-RESISTANT PLANTS OBTAINED
PATENT: WO 9909189-A 7 25-FEB-1999;
DEROSE RICHARD (FR): HOFFMANN JULES (FR)
LOCATION/QUALITIERS
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Derose, and Hoffmann, J.
GENE CODING FOR ANDROCTONINE, VECTOR CONTAINING SAME AND
TRANSFORMED DISEASE-RESISTANT PLANTS OBTAINED
PATENT: WO 9909189-A 6 25-FEB-1999;
DEROSE RICHARD (FR); HOFFMANN JULES (FR)
LOCATION/QUALIFIERS
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40.0%; Score 44; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 44; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 5.5e-22;
Matches 97; Conservative 0; Mismatches 0;
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/db_xref="taxon:32644"
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Sequence 9 from Patent W09924594.
A95931
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/db_xref="taxon:32644"
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Sequence 6 from Patent W09909189.
A98898 1 GI:6781860
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/db_xref="G1:10041014"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 169)
Lamberty, M., Hofmann, J., Bulet, P. and Brookhart, G.L.
Gene coding for heliomicine and use thereof
Patent: WO 9953053-A 2 21-0CT-1999;
LAMBERTY MIREILLE (FR); HOFWANN JULES (FR);
RHONE POULENC AGROCHIMIE (FR);
BROOKHART GARY LEE (US)
1. 169
1 (bases 1 to 109)
Lamberty, M., Pofmann, J., Bulet, P. and Brookhart, G.L.
Gene coding for heliconicine and use thereof
Patent: WO 9953053-A 8 21-OCT-1999;
LAMBERTY MIRELILE (FR); HOFMANN JULES (FR); BULET PHILIPPE (FR);
RHONE POULENC AGROCHMIE (FR); BROOKHART GARY LEE (US)
Location/Qualifiers
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/db_xref="taxon:32630"
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Sequence 3 from Patent W09953053.
AX014748
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Sequence 2 from Patent WO9953053.
AX014747
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         1 (Bases 1 to 87)
Derose,R. and Hoffmann,J.
Derose,R. and Hoffmann,J.
DEROSE,R. and Hoffmann,J.
TRANSFORMED DISEASE-RESISTANT PLANTS
PATENT: WO 9924594-A 9 20-MAY-1999,
DEROSE RICHARD (FR); HOFFMANN JÜLES (FR)
LOCALION/Qualifiers
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Derose, R. and Hoffmann, J.
Derose, R. and Hoffmann, J.
GENE CODING FOR THANATIN, VECTOR CONTAINING SAME AND RESULTING
TRANSFORMED DISEASE-RESISTANT PLANTS
PATENT: WO 924454-A 3 20-MAY-1999,
DEROSE RICHARD (FR); HOFFWANN JULES (FR)
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100.0%; Pred. No. 0.33;
iive 0; Mismatches
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0.33;
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A95925
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Sequence 8 from Patent W09953053.
AX014753
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/note="unnamed protein
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Gaps

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07-SEP-2000

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VRL 01-NOV-2000 VRL 01-NOV-2000 VRL 01-NOV-2000 VRL NOV-2000 VRD protein, early E3B 14.5 VDB protein genes, complete cds. AF086568
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AF086569/c AF086569 1430 bp DNA VRL 01-NOV-2000
LOCUS AF086569 1430 bp DNA VRL 01-NOV-2000
DEFINITION Human adenovirus type 37 early E3B 10.4 kba protein, early E3B 14.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MIPRFFLENILFCLENICAAFAAVSHASPDCLGPFPTYLLFALL
TCTCVCSIVCLVITFLQLIDWCCARYNYLHHSPERRDKNVARILRLI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="wtbHtlDLEMDGQASEQRILQLRVRQQQERAAKELLDAINIHQC
KKGIFCLVKQAKITYELVSNGKQHRLTYEMPQQKQKFTCMVGVNPIVITQQSGETNGC
THCSCESPECIYSLLKTLGCLRDLLFMN"
THCSCESPECIYSLLKTCGLRDLLFMN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MQTLLMLLSLLSPALATYADYSKCKFADIWNFLDCYQEKIDMPS YYLVIVGIVMVCSCTFFAIMIYPCFDLGWNSVEAFTYTLESSSLASTPPPPTRNQ
                                                                                                                                                                              Human adenovirus type 19.

Human adenovirus type 19

Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

1 (Abana viruses)

1 (Abana viruses)

Burgert, H. G. and Blusch, J. H.

Immunomodulatory functions encoded by the E3 transcription unit of
                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1430)
Blusch, J.H. and Burgert, H.-G.
Direct Submission
Submitted (25-AuG-1998) Virology, Max-von-Pettenkofer-Institute,
Submission
Location/Qualifiers
1. 1430
/organism="Human adenovirus type 19"
/db_xref="taxon:28278"
/note="number 86858 as described by Wadell, G. and de
Jong, J.C. Infection. Imun., 27, 292-296, 1980
subtype: Ad19a"
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/protein_id="AAF31742.1"
/db_xref="G1:6940696"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="carly E3B 14.7 kDa protein"
/protein_id="AAR31743.1"
/db_xref="G1:6940697"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/product="early E3B 10.4 kDa protein"
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Pred. No. 4.8;
0; Mismatches
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Best Local Similarity 56.9%;
Matches 58; Conservative 0
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AF086568/c
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                                                   DEFINITION
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                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
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TGKCQRM"
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                         1 (bases 1 to 261)
Lamberty, M. Hofmann, J., Bulet, P. and Brookhart, G.L.
Gene coding for heliomicine and use thereof
Patent: WO 9953053-A 3 21-OCT-1999;
LAMBERTY MIREILLE (FR): HOFMANN JULES (FR): BULET PHILIPPE (FR);
RHONE POULENC AGROCHIMIE (FR); BROOKHART GARY LEE (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 197)
Derose, R. and Hoffmann, J.
BEROSE, R. and Hoffmann, J.
ERNE CODING FOR THANATIN, VECTOR CONTAINING SAME AND RESULTING
TRANSFORMED DISEASE-RESISTANT PLANTS
PATENT: WO 924494-A 5 20-MAY-1999;
DEROSE RICHARD (FR); HOFFWANN JULES (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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/note="unnamed protein product"
                                                                                                                                                                                                             1. .261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12. .167 /note="unnamed protein product"
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Pred. No. 0.73;
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1.6;
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Seguence 5 from Patent W09924594.
A95927
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                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                         REFERENCE
AUTHORS
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JOURNAL
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TITLE
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GMEEIKGTVKVYPLPHMPVVKDLYPDLSNFYAQHRSIEPMLKTVSPTPAKEWKQSHED
RAKLDGLYEGILCACGSTSCPSYWWNGDRYLGPAVLLQAYRWLIDSRDEATGERLDNL
COMPILEMENT INNCAQACPKGINPAKAIAEIKKMMVERRV"
/Gene="AGR_C_4792"
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SADARFDGTTNSGQPLSLSR"
comptement(825..1604)
/gene="AGR_C_479p"
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YLVNNSGGREFWERTAPSAKDLASRDVVSRCWTWEIREGRGYGKNKGHIEFHLUHLDHD
ILHERLPGISESRAKIFAGVDYTREPIPVYNNGGIPTNYWGEVLNADANNPERI
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DRIMERFNSDERTANGSTPAVLEBUKNORAMODAAVPRTOSELESGORLGAIWRELP
DNK VTDRSWWWSDLVETLELHIMAANITTYYGABARKESGRGSHREDFVDGFGGR
DDVNWRKHTLANVSPEGDVKLDYRPVHTDLIADGIDPKKIEPKARVY"
                    Agrobacterium tumefaciens.
Agrobacterium tumefaciens
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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/gene="AGR_C_4790"
/note="ARP07569) succinate dehydrogenase iron-sulfur
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/gene="AGR_C_4792"
/note="SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT"
                                                                                                                                                                                                                                                                                            Unpublished
(hases 1 to 10344)
Hinkle, G., Slater, S.C. and Goodner, B.
Direct Submission
Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street, Cambridge, MA 02139, USA
                                                                                                                      1 (bases 1 to 10344)
Hinkle,G., Slater,S.C. and Goodner,B.
Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown Disease in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(77. .619)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. 10344
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complement(77. 619)
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                       SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"early E3B.10.4 kDa protein"
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HIGSCESPECIYSLLKTLGGLRDLLPNN"
1 474 c 275 g 353 t
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                                                                                                                                    Human adenovirus type 37.

Human adenovirus type 37

Yituses, dsDAN viruses, no RNA stage; Adenoviridae; Mastadenovirus.

1 (bases 1 to 1430)

Burgert, H.G. and Blusch, J. H.

Immunomodulatory functions encoded by the E3 transcription unit of
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Agrobacterium tumefaciens strain C58 circular chromosome, section
236 of the complete sequence.
AE008178 AE007869
AE008178.1 GI:15157847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Max-von-Pettenkofer-Institute,
kDa protein, and early E3B 14.7 kDa protein genes, complete cds.
ARO86569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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1. .276
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Blusch, J.H. and Burgert, H.-G.
Direct Submission
Submitted (25-AGC-1998) Virology, Max-von-Pr
Feodor Lynen Str. 25, Munich 81377, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    Virus Genes 21 (1-2), 13-25 (2000) 20475623 11022786
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Matches 58; Conservative
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complement (7395 . 8495)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MLFAFICKDKPGHLNVRMETRPAHLEHLNRLNAEGTLKIAGPFL
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HOMO Sapiens clone RP11-11K15, WORKING DRAFT SEQUENCE, 20 unordered
pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                         complement(6412. 7395)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.8%; Score 30.6; DB 1; Length 10344; ilarity 62.3%; Pred. No. 11; Conservative 0; Mismatches 29; Indels 0;
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/gene-"AGR_C_4808"
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8566. .qaae
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AC012145,4 GI:10047746
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                   dehydrogenase"
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riskHabnabaagay
complement(4929.__5573)
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complement(3469. .3849)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jene="AGR_C_4799". 5573)
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complement(6031. .6324)
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4551. .4928
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ORIGIN
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                                                                                  ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter code: Wisk

Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center clone name: 11.K.15
Center clone name: 11.K.15
Sequencing vector: Mi3; M7815; 100% of reads
Centersty: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 134421 bases at least Q40
Consensus quality: 140777 bases at least Q30
Consensus quality: 143656 bases at least Q30
Insert size: 157000; agarose-fp
Insert size: 157000; agarose-fp
Cuality coverage: 4.2 in Q20 bases; sum-of-contigs
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 148975)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo, sapiens, clone RP11-11K15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 bp
of 1104 bp in length
100 bp
of 2232 bp in length
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472 571 aga of 100 bp

572 1633: contig of 1062 bp in length

1634 1733: gap of 100 bp

1134 3114: contig of 1381 bp in length

3115 3214: gap of 100 bp

3115 3214: contig of 1727 bp in length
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12009 17154: contig of 5146 bp in length
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6145: cont
6245: gap of
8477: cont
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4942
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COMMENT

us-09-486-094-1.rge

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Unknown.
Unclassified.
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I (bases 1 to 246240)
Feder,J.Nathan, Kronmal,G.Scott, Lauer,P.M., Ruddy,D.A., Thomas,W., Tsuchinhashiz.a. and Wolff,R.K.
Megabase transcript map: novel sequences and antibodies thereto Patent: US 5872237-A 20 16-FEB-1999;
Patent: US 5872237-A 20 16-FEB-1999;
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Sequence 20 from patent US 5872237.
AR036572 GI:5953240
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LOCUS
DEFINITION
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AUTHORS
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JOURNAL
FEATURES
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Search completed: April 2, 2002, 21:29:29 Job time: 9641 sec